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MPSrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm  
on: Fri May 14 08:07:02 1999; MasPar time 158.91 Seconds  
Regular output not generated. 861.291 Million cell updates/sec  
Title: >US-08-911-423-3  
Description: (1-1006) from US08911423.seq  
Perfect Score: 1006  
N.A. Sequence: 1 ATGGCAGACACAGGGCGCAT.....ACACGTCCTGACTGGGAAA 1006  
Comp: TACCGTGTGTCGCCGCTA.....TGTTGAGGAGTACCCCTTT  
Scoring table: TABLE default  
Gap 6  
Nmatch STD : Dbase 0; Query 0  
Searched: 188442 seqs, 68026449 bases x 2  
Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Database: n-geneseq32  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29 30:part30 31:part31 32:part32 33:part33  
34:part34 35:part35 36:part36 37:part37 38:part38  
39:part39 40:part40  
Statistics: Mean 8.82; Variance 5.749; scale 1.547  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.  
SUMMARIES  
Result No. Score Query Match Length DB ID Description Pred. No.  
C 1 114 11.3 3327 30 T69936 Coprinus cinereus lac 1.47e-52  
2 96 9.5 2606 14 Q8327 P. falciparum E3la ge 2.05e-41  
3 96 9.5 2606 32 T72895 Plasmodium E3la gene. 2.05e-41  
4 85 8.4 1581 22 T32233 Cuphea C14:0-ACP thio 1.08e-34  
5 71 7.1 533 38 V02890 Human HMGI-C aberrant 2.80e-26  
6 65 6.5 774 38 V02893 Human HMGI-C aberrant 9.86e-23  
7 59 5.9 757 38 V02898 Human HMGI-C aberrant 3.12e-19  
8 43 4.3 91 9 Q51746 Oligonucleotide probe 3.27e-10  
C 9 42 4.2 91 9 Q51746 Oligonucleotide probe 3.27e-10  
10 42 4.2 204 1 N81164 Base substituted E.co 1.14e-09  
11 41 4.1 178 32 T76405 Human endothelin-1 an 3.97e-09  
12 39 3.9 204 1 N81164 Base substituted E.co 4.59e-08  
13 39 3.9 206 23 T27594 pGEM3zf target fragme 4.69e-08

Release 3.1A John F. Collins, Biocomputing Research Unit.  
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Gap 6

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1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29 30:part30 31:part31 32:part32 33:part33  
34:part34 35:part35 36:part36 37:part37 38:part38  
39:part39 40:part40

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6 65 6.5 774 38 V02893 Human HMGI-C aberrant 9.86e-23  
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12 39 3.9 204 1 N81164 Base substituted E.co 4.59e-08  
13 39 3.9 206 23 T27594 pGEM3zf target fragme 4.69e-08

C 14 39 3.9 206 37 T70340 DNA substrate for 5' 4.69e-08  
C 15 39 3.9 228 13 Q80775 5' Nuclease substrate 4.69e-08  
C 16 39 3.9 349 23 T27571 Human TSH beta-chain 4.69e-08  
17 39 3.9 969 40 T99561 Polynucleotide encodi 4.69e-08  
18 39 3.9 1287 3 N40087 Sequence from phage M 4.69e-08  
19 39 3.9 1287 3 N50326 Phage M13tg910 used i 4.69e-08  
20 39 3.9 1380 2 Q11381 T. hyo gene 6:lacZ fu 4.69e-08  
21 39 3.9 1619 12 Q71364 Expression cassette c 4.69e-08  
22 39 3.9 1754 12 Q71365 Expression cassette c 4.69e-08  
23 39 3.9 2027 25 T42137 I2C-4 gene encoding F 4.69e-08  
C 24 39 3.9 3198 38 T92869 Candida carhol gene. 4.69e-08  
C 25 39 3.9 3212 40 V03313 Archaeoglobus lithotr 4.69e-08  
C 26 39 3.9 3681 2 Q13578 Plasmid pKSEL5. 4.69e-08  
C 27 39 3.9 3699 39 V14340 Plasmid pBSGFP expres 4.69e-08  
C 28 39 3.9 4118 35 T59189 Construct pGEM-htr(Ka 4.69e-08  
C 29 39 3.9 4118 35 T59188 Construct pGEM-htr co 4.69e-08  
C 30 39 3.9 4164 16 T04575 Plasmid pAT-1 sequenc 4.69e-08  
C 31 39 3.9 4274 9 Q54144 Sequence of plasmid p 4.69e-08  
C 32 39 3.9 4283 37 T86610 Epidermal growth fact 4.69e-08  
C 33 39 3.9 4283 35 T86449 DNA encoding hGH, EGF 4.69e-08  
C 34 39 3.9 4539 14 Q87347 Plasmid pINVI. 4.69e-08  
C 35 39 3.9 4771 38 V02186 Human type C lectin e 4.69e-08  
C 36 39 3.9 4792 15 Q84696 Plasmid GS contg. N. 4.69e-08  
C 37 39 3.9 4933 16 T04569 Plasmid pAT-2 sequenc 4.69e-08  
C 38 39 3.9 5042 15 Q84694 Plasmid glucoamylase 4.69e-08  
C 39 39 3.9 6824 6 Q39050 K.lactis/S. cerevisae 4.69e-08  
40 39 3.9 7287 39 V02042 Plasmid pWRG3169 enco 4.69e-08  
41 39 3.9 9837 38 T96851 Intron 21 of human pR 4.69e-08  
C 42 39 3.9 10306 12 Q73734 Retro virus vector p5 4.69e-08  
C 43 39 3.9 10930 20 Q81226 Plasmid pMI6-1. 4.69e-08  
C 44 39 3.9 10950 20 Q81225 Plasmid pMI6. 4.69e-08  
45 39 3.9 10970 12 Q73735 Retro virus vector p5 4.69e-08

ALIGNMENTS

RESULT 1  
ID T69936 standard; DNA; 3327 BP.  
AC T69936;  
DT 21-JUL-1997 (first entry)  
DE Coprinus cinereus lacase lcc1 genomic DNA.  
KW Benzenediol:oxygen oxidoreductase; lacase; lignin; Kraft pulp; dye;  
KW fungus; polymerase chain reaction; papermaking; ss.  
OS Coprinus cinereus (strain IFO 8371).  
FH Key Location/Qualifiers  
FT exon 1..851  
FT /\*tag= a  
FT /number= 1  
FT /codon\_start= 725  
FT intron 852..906  
FT /\*tag= b  
FT /number= 1  
FT /cons\_splice= (5'site:YES,3'site:YES)  
FT /note= "The printed version of the sequence has the  
FT following splice junction sequences (with  
FT exon nucleotides shown in capitals and intron  
FT nucleotides shown in lower case):  
FT 5' site:GC/gt and 3' site:ag/tg"  
FT exon 907..1023  
FT /\*tag= c  
FT /number= 2  
FT intron 1024..1100  
FT /\*tag= d  
FT /number= 2  
FT /cons\_splice= (5'site:YES,3'site:YES)  
FT /note= "The printed version of the sequence has the  
FT following splice junction sequences (with  
FT exon nucleotides shown in lower case):  
FT 5' site:GC/gt and 3' site:ag/tg"  
FT exon 1101..1248  
FT /\*tag= e  
FT /number= 3  
FT intron 1249..1316  
FT /\*tag= f  
FT /number= 3  
FT /cons\_splice= (5'site:NO,3'site:NO)  
FT /note= "The printed version of the sequence has the



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RESULT 3
ID T72895 standard; cDNA; 2606 BP.
AC T72895;
DT 07-OCT-1997 (first entry)
DE Plasmodium E31a gene.
KW DBL gene family; SABP; sialic acid binding protein; vaccine; therapy;
KW Duffy binding like gene; Duffy antigen binding protein; erythrocyte;
KW DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune response;
KW Plasmodium; ss.
OS Plasmodium falciparum.
FH Key Location/Qualifiers
FT cds 106..2460
FT /tag= a
FT /note= *encodes residues 1-785 of W22480*
PN W09640766-A2.
PD 19-DEC-1996.
PF 07-JUN-1995; U09508.
PR (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI Chitnis C, Miller LH, Peterson DS, Sim KL, Su X;
PI Wellem's TE;
DR WPI: 97-052231/05.
DR P-PSDB; W22480.
PT New malaria vaccines - contains cysteine-rich DBL family protein
PT binding domains homologous domains of the Duffy and sialic acid
PT binding proteins
PS Disclosure; Page 43; 96pp; English.
CC This sequence represents the E31a gene of Plasmodium. E31a belongs to
CC the Duffy binding like (DBL) family of genes which have homology to the
CC Duffy antigen binding protein (DABP) and sialic acid binding protein
CC (SABP) conserved regions (see T72889 and T72888 respectively). The var
CC family of genes modulate cytoadherence and antigenic variation of
CC Plasmodium infected erythrocytes. SABP and the Duffy antigen binding
CC protein (DABP) are soluble proteins that appear in the culture
CC supernatant after infected erythrocytes release merozoites. DABP and SABP
CC mediate the binding of merozoites and schizonts to the erythrocyte
CC surface. These proteins are necessary for erythrocyte invasion by the
CC parasite. This sequence can be used in the compositions of the invention.
CC The compositions are for the treatment and prevention of malaria, and
CC comprise either a nucleotide sequence or encoded polypeptide of the
CC var-1, var-2, var-3 or var-7 genes of the DBL gene family, a family of
CC genes having homology with conserved regions of DABP and SABP. The
CC compositions are used for the treatment and prevention of malaria. They
CC are also used in the preparation of vaccines for inducing a protective
CC immune response in a mammal to Plasmodium merozoites (especially
CC Plasmodium falciparum or Plasmodium vivax).
CC Sequence 2606 BP; 992 A; 351 C; 569 G; 694 T;
CC Query Match 9.5%; Score 96; DB 32; Length 2606;
CC Best Local Similarity 99.0%; Pred. No. 2.05e-41;
CC Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Dd 2455 caagctacgctgcatcgacgtcatagctcttcttagtgcacctaaattcaa 2514
|||||
Qy 909 CAAGCTTAGGTACGGTGCATCGGACGTCATAGCTTCTTATAGTGTCACTCAATTCAA 968
|||||

Dd 2515 ttaactggcgtcgcttttacaacgtcgactgggaaa 2552
|||||
Qy 969 TTCACGTGGCGTCGTTTACACACGCTCCTGACTGGGAAA 1006
|||||

RESULT 4
ID T32233 standard; cDNA; 1581 BP.
AC T32233;
DT 26-OCT-1996 (first entry)
DE Cuphea C14:0-ACP thioesterase cDNA clone MCT34 (CpFatB2).
KW Myristate; myristic acid; fatty acid; acyl-ACP thioesterase;
KW seed oil; oilseed; vegetable oil; Brassica; transgenic plant;
KW surfactant; ss.
OS Cuphea palustris.
FH Key Location/Qualifiers
FT cds 119..1354

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FT W09623892-A2.
PN 08-AUG-1996.
PD 01-FEB-1996; U01585.
PF 02-FEB-1995; US-383756.
PR 05-JUN-1995; US-460898.
PA (CALJ ) CALGENE INC.
PI Dehesh K, Hawkins D, Voelker TA;
DR WPI: 96-371439/37.
DR P-PSDB; W02081.
PT Recombinant prodn. of myristate in plant cells - using DNA with
PT preferential activity on C14 fatty acids from Cuphea palustris,
PT nutmeg and camphor, useful in detergent and food industries
PS Example 1; Fig 1A-1E; 77pp; English.
CC A cDNA clone (T32233), designated MCT34 (pCpFatB2), codes for Cuphea
CC palustris C14:0-ACP thioesterase (W02081), an enzyme that acts
CC primarily on C14:0-ACP substrates, forming C14:0 (myristate). It
CC was isolated from a developing seed cDNA library by screening with
CC sequences encoding medium-chain acyl-ACP thioesterases from Cuphea
CC hookeriana. Constructs for expression of clone MCT34 in plant seeds
CC under the control of napin or oleosin regulatory regions were prepd.
CC These allow high-level prodn. of myristate (useful in surfactants
CC and foods) in plant cells, e.g. Brassica.
CC Sequence 1581 BP; 418 A; 356 C; 410 G; 397 T;
CC Query Match 8.4%; Score 85; DB 22; Length 1581;
CC Best Local Similarity 98.9%; Pred. No. 1.08e-34;
CC Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Dd 1495 ggcggcgctctagaggatccaagcttaacgctgacgtgcacgtcatagctcttct 1554
|||||
Qy 889 GGGGGCGGCTCTAAAGATCCCAAGCTTACGTACGCGTGCGTGCATGCTCTCTCT 948
|||||

Dd 1555 atagtgcacctaaattcaattcaactg 1581
|||||
Qy 949 ATAGTGTCACTAAATTCATTCACGTG 975
|||||

RESULT 5
ID V02890 standard; cDNA; 533 BP.
AC V02890;
DT 08-MAY-1998 (first entry)
DE Human HMGI-C aberrant form 11.
KW High mobility group protein; HMGI-C; MAG; human; treatment; modulator;
KW multiple tumour aberration growth gene; vascular development;
KW angiogenesis; vascularisation; endometriosis; contraception
KW tissue regeneration; ss.
OS Homo sapiens.
PN DE19548122-A1.
PD 26-JUN-1997.
PF 21-DEC-1995; 048122.
PR 21-DEC-1995; DE-048122.
PA (BULL/) BULLERDIEK J.
PI Bullerdiek J;
DR WPI: 97-333837/31.
PT DNA sequences representing aberrant forms of human high mobility
PT group protein genes - useful for treatment of endometriosis and
PT tumours, or for modulating vascularisation, etc
PS Claim 1; Fig 11; 58pp; German.
CC V02880-V02898 are cDNA sequences that encode aberrant forms of the human
CC high mobility group protein (HMG) gene, HMGI-C, which is located on
CC chromosome 12. These sequences encode the DNA binding part of the
CC translation product but not the protein binding domain. These proteins,
CC antibodies derived from these proteins or expression modulators of the
CC HMGI-C protein can be used in kits to modulate vascular development. Such
CC kits can reduce, block or stimulate angiogenesis or vascularisation and
CC can improve vascular provision in myocardium damaged by infarction. Such
CC proteins can also be used to treat endometriosis and tumours, for
CC contraception (local or oral) and for tissue regeneration, especially in
CC degenerating or damaged tissue. The regeneration method can be applied to
CC tissues which are currently impossible or difficult to regenerate and the
CC use of biological material with attendant risks of viral transmission and
CC anaphylactic shock, is avoided.

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SQ Sequence 533 BP; 175 A; 146 C; 127 G; 85 T;  
 Query Match 7.1%; Score 71; DB 38; Length 533;  
 Best Local Similarity 98.6%; Pred. No. 2.80e-26;  
 Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

D 461 ggccgctctagagattccaaagcttacgtacgtgcgtacgtacgtacgtctctct 520  
 |||||  
 QY 889 GCGGGCGCTCTAAAGATCCAAAGCTTACGTACGCGTGCATGGACGTCTAGCTCTCT 948

D 521 atagtgtcaccta 533  
 |||||  
 QY 949 ATAGTGTACCTA 961

RESULT 6  
 ID V02883 standard; cDNA; 774 BP.  
 AC V02883;  
 DT 08-MAY-1998 (first entry)  
 DE Human HMGI-C aberrant form 4.  
 KW High mobility group protein; HMGI-C; MAG; human; treatment; modulator;  
 KW multiple tumour aberration growth gene; vascular development;  
 KW angiogenesis; vascularisation; endometriosis; contraception  
 OS Homo sapiens.  
 PN DE19548122-A1.  
 PD 26-JUN-1997.  
 PF 21-DEC-1995; 048122.  
 PA (BULL/) BULLERDIEK J.  
 PI Bullerdiek J;  
 DR WPI: 97-333837/31.

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 CC contraception (local or oral) and for tissue regeneration, especially in  
 CC degenerating or damaged tissue. The regeneration method can be applied to  
 CC tissues which are currently impossible or difficult to regenerate and the  
 CC use of biological material with attendant risks of viral transmission and  
 CC anaphylactic shock, is avoided.  
 SQ Sequence 774 BP; 235 A; 205 C; 163 G; 171 T;

Query Match 6.5%; Score 65; DB 38; Length 774;  
 Best Local Similarity 98.5%; Pred. No. 9.86e-23;  
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

D 708 ggccgctctagagattccaaagcttacgtacgtgcgtacgtacgtacgtctctct 767  
 |||||  
 QY 889 GCGGGCGCTCTAAAGATCCAAAGCTTACGTACGCGTGCATGGACGTCTAGCTCTCT 948

D 768 atagtgt 774  
 |||||  
 QY 949 ATAGTGT 955

RESULT 7  
 ID V02898 standard; cDNA; 797 BP.  
 AC V02898;  
 DT 08-MAY-1998 (first entry)  
 DE Human HMGI-C aberrant form 19.  
 KW High mobility group protein; HMGI-C; MAG; human; treatment; modulator;  
 KW multiple tumour aberration growth gene; vascular development;  
 KW angiogenesis; vascularisation; endometriosis; contraception

KW tissue regeneration; ss.  
 OS Homo sapiens.  
 PN DE19548122-A1.  
 PD 26-JUN-1997.  
 PF 21-DEC-1995; 048122.  
 PR 21-DEC-1995; DE-048122.  
 PA (BULL/) BULLERDIEK J.  
 PI Bullerdiek J;  
 DR WPI: 97-333837/31.

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 CC proteins can also be used to treat endometriosis and tumours, for  
 CC contraception (local or oral) and for tissue regeneration, especially in  
 CC degenerating or damaged tissue. The regeneration method can be applied to  
 CC tissues which are currently impossible or difficult to regenerate and the  
 CC use of biological material with attendant risks of viral transmission and  
 CC anaphylactic shock, is avoided.  
 SQ Sequence 797 BP; 267 A; 178 C; 181 G; 167 T;

Query Match 5.9%; Score 59; DB 38; Length 797;  
 Best Local Similarity 96.8%; Pred. No. 3.12e-19;  
 Matches 61; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

D 735 ggccgctctagagattccaaagcttacgtacgtgcgtacgtacgtacgtctctct 794  
 |||||  
 QY 889 GCGGGCGCTCTAAAGATCCAAAGCTTACGTACGCGTGCATGGACGTCTAGCTCTCT 948

D 795 ata 797  
 |||  
 QY 949 ATA 951

RESULT 8  
 ID Q51746 standard; cDNA; 91 BP.  
 AC Q51746;  
 DT 31-MAY-1994 (first entry)  
 DE Oligonucleotide probe MK14-A  
 KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;  
 KW ss. Synthetic.  
 OS Synthetic.  
 PN EP-571911-A.  
 PD 01-DEC-1993.  
 PF 24-MAY-1993; 108325.  
 PR 26-MAY-1992; US-889651.  
 PA (BECT ) BECTON DICKINSON CO.  
 PI Shank DD, Spears PA;  
 DR WPI: 93-37884/48.

PT New oligo:nucleotide probes specific for Mycobacteria - used for  
 PT detection and amplification of Mycobacteria nucleic acid in  
 PT samples  
 PS Claim 3; Page 14; 23pp; English.  
 CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14  
 CC (Q51735). It hybridized to all spp. of mycobacteria tested, but  
 CC cross reacted to a few non-mycobacterial spp. The probe may  
 CC be useful as an initial screen for mycobacterial infection.  
 CC See also Q51735-45 and Q51747-59.  
 SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

Query Match 4.3%; Score 43; DB 9; Length 91;  
 Best Local Similarity 12.7%; Pred. No. 3.27e-10;  
 Matches 8; Conservative 45; Mismatches 10; Indels 0; Gaps 0;

D 1 ggctccggcgssvhsyyvvhvshhshvshhshvshhshvshhshvshhshvshhshvshhshvsv 60





CC DNA-polymerases to cleave a specific sequence structure  
 CC was tested using the duplex sequence given in Q80775 and  
 CC the pilot oligonucleotides given in Q80758-60.  
 SQ Sequence 228 BP; 59 A; 56 C; 53 G; 60 T;  
 Query Match 3.9%; Score 39; DB 13; Length 228;  
 Best Local Similarity 97.6%; Pred. No. 4.69e-08;  
 Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Db 10 ttccccagtcacgacgttgtataaacgacgacgcccagtggaattg 50  
 ||||||||| |||||||||||||||||||||||||  
 Cp 1006 TTCCCGAGTCAGGACGTTGTAAACGACGCGCCAGTGAATTG 966

Search completed: Fri May 14 08:09:48 1999  
 Job time : 166 secs.

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MPSrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm  
on: Fri May 14 07:16:35 1999; MasPar time 1611.89 Seconds  
1474.893 Million cell updates/sec  
Regular output not generated.

Title: >US-08-911-423-3  
Description: (1-1006) from US08911423.seq  
Perfect Score: 1006  
N.A. Sequence: 1 ATGCACAGCAGCGGGCGAT.....ACACGCTCTGACTGGGAAA 1006  
Comp: TACCGTGTGTCGCCCGCTA.....TGTTCAGGACTGACCCCTT

Scoring table:  
Gap 6  
TABLE default

Nmatch STD : Dbase 0; Query 0

Searched: 602357 seqs, 1181590623 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: emb157  
1:em\_ba 2:em\_fun 3:em\_htg 4:em\_hum1 5:em\_hum2 6:em\_in  
7:em\_om 8:em\_or 9:em\_ov 10:em\_pat 11:em\_ph 12:em\_pl  
13:em\_ro 14:em\_un 15:em\_vi

Database: genbank110  
16:gb\_ba1 17:gb\_ba2 18:gb\_htg 19:gb\_in 20:gb\_om 21:gb\_ov  
22:gb\_pat 23:gb\_ph 24:gb\_pl1 25:gb\_pl2 26:gb\_pr1  
27:gb\_pr2 28:gb\_pr3 29:gb\_ro 30:gb\_st 31:gb\_sts 32:gb\_sy  
33:gb\_un 34:gb\_vi

Statistics: Mean 10.691; Variance 5.553; scale 1.925

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description	Pred. No.
1	228	22.7	1020 29	MMU82534 Mus musculus glucocort	2.35e-151
2	116	11.5	4109 33	PSPORT1 Cloning vector pSport1	1.95e-63
3	106	10.5	4310 33	XXU12391 Cloning vector pSport2	7.72e-56
4	85	8.4	1581 22	I60018 Sequence 1 from patent	3.80e-40
5	82	8.2	5772 24	SCU15970 Saccharomyces cerevisi	6.09e-38
6	70	7.0	2699 34	HIV-1 strain M02 from	3.04e-29
7	68	6.8	98 27	HUMD4H12M3 Human HepG2 3' region	8.14e-28
8	63	6.3	538 22	AR023813 Sequence 1 from patent	2.80e-24
9	59	5.9	398 31	GI3951 human STS SHGC-2867 cl	1.74e-21
10	58	5.8	433 31	G41212 LSCV119 Caprine BAC Ca	8.55e-21
11	57	5.7	3160 32	PSVSPORT Cloning vector pSVSPOR	4.19e-20
12	56	5.6	1297 24	CSPATATLP Cucumis sativus mRNA f	2.04e-19
13	55	5.5	414 31	G4155 human STS SHGC-6182 cl	9.85e-19

C	14	55	2746 32	CVPGEM42	Cloning vector pGEM-42	9.85e-19
	15	54	390 31	G16894	human STS SHGC-3196 cl	4.74e-18
	16	48	412 31	G17976	human STS SHGC-3315 cl	5.04e-14
	17	48	7218 22	I66494	Sequence 14 from patent	5.04e-14
	18	45	1359 29	MUSHAPTGB	Mus saxicola haptoglob	4.68e-12
	19	44	965 22	AR024229	Sequence 22 from patent	2.08e-11
	20	41	215 22	I28278	Sequence 5 from patent	1.72e-09
	21	41	346 31	G41210	LSCV116 Caprine BAC Ca	1.72e-09
	22	41	7218 22	I66494	Sequence 14 from patent	1.72e-09
C	23	40	2860 32	AF017063	Cloning vector pMEK19	7.32e-09
	24	40	4498 16	ECY10544	Cloning vector pKEL194	7.32e-09
	25	39	1287 22	A04663	Phage M13tg910	3.08e-08
C	26	39	2886 19	CPU69698	Cryptosporidium parvum	3.08e-08
	27	39	2958 32	ARBLKSP	pBluescript KS(+) vect	3.08e-08
C	28	39	2958 32	ARBLKSP	pBluescript SK(+) vect	3.08e-08
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C	30	39	3223 32	CVGEM112P	Cloning vector pGEM-11	3.08e-08
C	31	39	3570 32	CVU39779	Cloning vector pTRIPLE	3.08e-08
	32	39	4091 19	PL18SRNA	P.lividus gene for l8S	3.08e-08
C	33	39	4190 32	XXU13848	pEXCell cloning vector	3.08e-08
	34	39	4539 22	I18794	Sequence 1 from patent	3.08e-08
C	35	39	4670 24	ATHAVPEA	Arabidopsis thaliana g	3.08e-08
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C	37	39	5314 22	A20700	pMTV1 DNA sequence	3.08e-08
C	38	39	5967 32	EVU84006	Expression vector pBSI	3.08e-08
C	39	39	6170 32	U02457	Cloning vector pYEBra3	3.08e-08
C	40	39	7372 32	SYNPHSCSKV	Phagescript SK cloning	3.08e-08
C	41	39	7507 32	CVU51113	Cloning vector pBeloBA	3.08e-08
C	42	39	21013 27	D78345	Human DNA for Ig gamma	3.08e-08
C	43	39	94882 18	AC002317	*** SQUENCING IN PROG	3.08e-08
C	44	39	167846 18	CEY56C5	Caenorhabditis elegans	3.08e-08
C	45	39	256175 18	HS437G10	Human DNA sequence ***	3.08e-08

ALIGNMENTS

RESULT	1	MMU82534	1020 bp	MRNA	ROD	18-OCT-1997
LOCUS		Mus musculus glucocorticoid induced TNFR family related protein precursor, mRNA, complete cds.				
DEFINITION						
ACCESSION		U82534				
NID		G2228583				
KEYWORDS		house mouse.				
SOURCE		Mus musculus				
ORGANISM		Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE		1 (bases 1 to 1020)				
AUTHORS		Nocentini,G., Giunchi,L., Ronchetti,S., Krausz,L.T., Bartoli,A., Moraca,R., Miglioni,G. and Ricciardi,C.				
TITLE		A new member of the tumor necrosis factor/nerve growth factor receptor family inhibits T cell receptor-induced apoptosis				
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 94 (12), 6216-6221 (1997)				
MEDLINE		97322352				
REFERENCE		2 (bases 1 to 1020)				
AUTHORS		Nocentini,G., Giunchi,L., Ronchetti,S., Krausz,L.T., Bartoli,A., Moraca,R., Miglioni,G. and Ricciardi,C.				
TITLE		Direct Submission				
JOURNAL		Submitted (18-DEC-1996) Carlo Ricciardi, Clinical Medicine, Pathology and Pharmacology, Perugia University, V. del Giochetto, Perugia, PG 06100, Italy				
FEATURES		Location/Qualifiers				
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		/cell_type="thymocytes"				
		46..732				
CDS		/note="type I transmembrane protein; belongs to the tumor necrosis factor receptor/nerve growth factor receptor family"				
		/codon_start=1				
		/product="glucocorticoid induced TNFR family related"				







partial cds.  
U84854  
g2290120

KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS

TITLE

JOURNAL  
MEDLINE  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

FEATURES  
source

gene

CDS

BASE COUNT  
ORIGIN

Query Match 7.0%; Score 70; DB 34; Length 2699;  
Best Local Similarity 98.6%; Pred. No. 3.04e-29;  
Matches 71; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 AGGTGACACTATAGAGAGCTATGACGTCGCATGCACGCGTAGCTTGGATCCTCT 60  
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Cp 960 AGGTGACACTATAGAGAGCTATGACGTCGCATGCACGCGTAGCTTGGATCCTCT 901  
Db 61 AGAGCGGCGGCC 72

Cp 900 AGAGCGCGCC 889  
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RESULT 7 HUMD4H12M3 98 bp mRNA PRI 01-DEC-1994  
LOCUS Human HepG2 3' region MboI cDNA, clone hmd4h12m3.  
DEFINITION D17247  
ACCESSION g598848  
NID gene signature.  
KEYWORDS Homo sapiens Male cell\_line:HepG2 cDNA to mRNA, clone\_lib:Kiseru.  
SOURCE Homo sapiens  
ORGANISM Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata;  
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;  
Homo.

REFERENCE 1 (bases 1 to 98)  
AUTHORS Matoba,K., Okubo,K., Hori,N., Fukushima,A. and Matsubara,K.  
TITLE The addition of 5'-coding information to a 3'-directed cDNA library  
ABSTRACT improves analysis of gene expression  
JOURNAL Gene 146 (2), 199-207 (1994)  
PUBLISHER 94357437

REFERENCE 2 (bases 1 to 98)  
AUTHORS Matoba,K.  
TITLE Direct Submission  
JOURNAL Submitted (21-JUL-1993) to the DDBJ/EMBL/GenBank databases. Ryo  
Matoba, Osaka University, Institute for Molecular and Cellular Bio;  
1-3, Yamada-oka, Suita, Osaka 565, Japan  
(E-mail:matoba@inherit.imcb.osaka-u.ac.jp,  
Tel:81-6-877-5111(ex.3314), Fax:81-6-877-1922)  
COMMENT Submitted (21-Jul-1993) to DDBJ by:  
Ryo Matoba  
Molecular Microbiology and Genetics Lab.  
Research Institute of Innovative technology for the Earth 9-2  
Kizugawadai Kizu-cho,  
Japan, 619-02  
Soraku-gun, Kyoto  
Phone: 07747-5-2308  
Fax: 07747-5-2321.

FEATURES  
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/db\_xref="taxon:9606"  
/cell\_line="HepG2"  
/clone\_lib="Kiseru"  
/sex="Male"  
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Matches 78; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 9 GCGCGCGCTCTAGAGGATCCAAAGCTTACGACGCGTGCATGCGACGTCATAGCTCTTCTA 68  
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Db 69 TAGANGCACCTTAATCAATCAACTGCGCC 97  
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Qy 950 TAGTGTACCTAAATTCATTCACCTGCGC 978

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LOCUS AR023813 538 bp DNA PAT 04-DEC-1998  
DEFINITION Sequence 1 from patent US 5795740.  
ACCESSION AR023813  
NID g3977107  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 538)  
AUTHORS Platika,M., Platika,O. and Holland,J.F.  
TITLE Pituitary differentiation factor and methods of use thereof

JOURNAL Patent: US 5795740-A 1 18-AUG-1998;  
FEATURES Location/Qualifiers  
source 1..538  
/organism="unknown"

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Matches 83; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

Db 441 GCGCGCGCTCTAGAGGATCCAAAGCTTACGACGCGTGCATGCGACGTCATNN-TCTTCTT 499  
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Qy 890 GCGCGCGCTCTAAGAGATCCAAAGCTTACGACGCGTGCATGCGACGTCATGCTTCTA 949  
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Db 500 TAGTGTCAACCTAAATCAAT-CANTGGCGCGCGTT 534  
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Qy 950 TAGTGTCACTAAATTCATTCACCTGCGCGTGT 985

RESULT 9  
LOCUS GI13951 398 bp DNA STS 22-DEC-1995  
DEFINITION human STS SHGC-2867 clone pg-564.  
ACCESSION GI13951  
NID g1129690  
KEYWORDS STS sequence; primer; sequence tagged site.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;  
Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 398)  
AUTHORS Myers,R.M.  
JOURNAL Unpublished (1995)  
COMMENT

Contact: Richard M. Myers  
Stanford Human Genome Center (SHGC)  
Stanford University School of Medicine  
Department of Genetics, M-344, Stanford, CA 94305, USA  
Tel: 4157259687  
Fax: 4157259689  
Email: myers@shgc.stanford.edu

Primer A: CTTCTGGCAGGCAATTTTCAATC  
Primer B: CAGGGTACTTTATCTCTAGCTC  
STS size: 132  
PCR Profile:

Initial incubation: 94 degrees C for 90 seconds  
Denaturation: 94 degrees C for 15 seconds  
Annealing: 62 degrees C for 23 seconds  
Polymerization: 72 degrees C for 30 seconds  
PCR Cycles: 30  
Thermal Cycler: Perkin Elmer 9600  
Protocol:  
Template: 25 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Taq Polymerase: 0.05 units/ul  
Total Vol: 10 ul

Buffer: MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.3

Plasmid clones, generated from a lymphoblastoid cell line from a  
human male. Localized to human chromosome 2 by analysis on the  
NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell Institute  
for Medical Research, Camden, NJ 08103.  
Location/Qualifiers

FEATURES

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Best Local Similarity 88.2%; Pred. No. 1.74e-21;
Matches 67; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
Db 320 GCGCGNCTCTAGAGATCCAAAGCTTACCTAGCGTGCATNGGANGTCATAG-TCTTCT 378
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QY 889 GCGCGCGCTCTAAGAGATCCAAAGCTTACCTAGCGTGCATNGGANGTCATAGCTTCT 948
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QY 949 ATAGTGTCACTAAAT 964
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Best Local Similarity 96.8%; Pred. No. 8.55e-21;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 945 TTCTATAGTGTCACTAAATTCACCTGCGCGTCTTTTACAACTGCTGACTGGGA 1004
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Db 352 AA 353
QY 1005 AA 1006
ORGANISM
REFERENCE
AUTHORS
Vainan,D., Schibler,L., Oustry-Vainan,A., Pailhoux,E., Furet,J.-P.,
Goldammer,T., Cotinot,C., Schwerin,M., Fellous,M. and Cribiu,E.P.
TITLE
High-resolution human/goat comparative map of the goat
Pooled/Intersex Syndrome (PIS): The human homologue is contained in
a human YAC from HSA3q23
JOURNAL
COMMENT
Unpublished (1999)
Contact: Edmond P. Cribiu
Laboratoire de Genetique biochimique et de Cytogetenetique
Institut National de la Recherche Agronomique
Centre de Recherche INRA de Jouy-en-Josas, 78352 Jouy-en-Josas,
France
Tel: 33134652672
Fax: 33134652478
Email: cribie@biotec.jouy.inra.fr
Primer A: CAAGCTACAGTCTATAGGGTC
Primer B: CTACACTGGCCAGAGATTC
STS size: 155
PCR Profile:
Presoak: 94 °C for 5 minutes
Denaturation: 94 °C for 15 seconds
Annealing: 58 °C for 20 seconds
Polymerization: 72 °C for 20 seconds
PCR cycles: 30
Thermal cycler: MJ Research or Perkin-Elmer Cetus
Protocol:
Template: 30-100 ng
Primer: each 1 uM
dGTP, dCTP, dTTP: 100mM, dATP: 10mM + alpha P33 dATP 0.5 uCi
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul
Buffer:
MgCl2: 2 mM
(NH4)2SO4: 20mM
Tween20: 0.01% w/v
Tris-HCl: 75 mM
pH: 9

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/clone_lib="Caprine BAC"
/sex="male"
/tissue_type="skin"
/cell_type="fibroblast"
/cell_line="CAT2"
/dev_stage="adult"
71..225
primer_bind 71..91
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Query Match      5.8%; Score 58; DB 31; Length 433;
Best Local Similarity 96.8%; Pred. No. 8.55e-21;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 292 TTCTATAGTGTCACTAAATCCAAATTCACCTGCGCGTCTTTTACAACTGCTGACTGGGA 351
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Db 352 AA 353
QY 1005 AA 1006
ORGANISM
REFERENCE
LOCUS      PSVSPORT      3160 bp      DNA      circular      SYN      24-MAY-1995
DEFINITION Cloning vector pSVSport1 beta-lactamase gene, complete cds.
ACCESSION  U14626
NID         9540252
KEYWORDS
SOURCE      Cloning vector pSVSport1.
ORGANISM    Cloning vector pSVSport1
REFERENCE 1 (sites)
AUTHORS   D'Alessio,J.M.
TITLE     Life Technologies, Inc. Catalogue
JOURNAL   Unpublished (1994)
REFERENCE 2 (bases 1 to 3160)
AUTHORS   Horton,M.E.
TITLE     Direct Submission
JOURNAL   Submitted (12-SEP-1994) Mary E. Horton, Life Technologies, Inc.,
Technical Services, 8400 Helgeman Court, Gaithersburg, MD
20884-9980, USA
FEATURES
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Location/Qualifiers
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intron 586..723
polyA_signal 912..919
polyA_signal 941..948
rep_origin 1146..1170
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/evidence=experimental
/product="beta-lactamase"
/db_xref="PID:g540253"
/translation="MSIQHFRVALIPFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
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Cp 1006 TTTCCCAAGTCCAGGACGTTGTAAAAACGACGGCCAGTGAATTCGATTTAGTGACACTATA 948  
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 DEFINITION human STS SHGC-3196 clone pg-1108.  
 ACCESSION G16894  
 NID g1214320  
 KEYWORDS STS sequence; primer; sequence tagged site.  
 SOURCE human Plasmid clones, generated from a lymphoblastoid cell line from a human male. Localized to human chromosome 5 by analysis on the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell Institute for Medical Research, Camden, NJ 08103.  
 ORGANISM Homo sapiens  
 Eukaryoteae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonadata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 390)  
 AUTHORS Myers, R.M.  
 JOURNAL Unpublished (1996)  
 COMMENT  
 Contact: Richard M. Myers  
 Stanford Human Genome Center (SHGC)  
 Stanford University School of Medicine  
 Department of Genetics, M-344, Stanford, CA 94305, USA  
 Tel: 4157259687  
 Fax: 4157259689  
 Email: myers@shgc.stanford.edu  
 Primer A: TTGTTGATGATCTGGCATATGTTAG  
 Primer B: GGCCAAAAAAGCGAAGCTCCATC  
 SPS size: 130  
 PCR Profile:  
 Initial incubation: 94 degrees C for 90 seconds  
 Denaturation: 94 degrees C for 15 seconds  
 Annealing: 64 degrees C for 23 seconds  
 Polymerization: 72 degrees C for 30 seconds  
 PCR Cycles: 30  
 Thermal Cycler: Perkin Elmer 9600  
 Protocol:  
 Template: 25 ng  
 Primer: each 1 uM  
 dNTPs: each 200 uM  
 Taq Polymerase: 0.05 units/ul  
 Total Vol: 10 ul  
 Buffer:  
 MgCl2: 2.5 mM  
 KCl: 50 mM  
 Tris-HCl: 20 mM  
 pH: 8.3  
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 Matches 96; Conservative 0; Mismatches 10; Indels 6; Gaps 6;  
 Db 244 GCGGGCGNTCTAGAGGATCCCAAGCTTACGCGGTNCATGGCAGCTCATAGCTCTCC 303  
 Qy 889 GCGGCGCGCTCTAAGG-ATCCAAGCTTACGTAGCGGTGCATGGCAGCTCATAGCTCTTC 947

Search completed: Fri May 14 07:43:41 1999  
Job time : 1626 secs.